

RAW SEQUENCE LISTING

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Application Serial Number:

10/506,327

Source:

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/506,327

DATE: 04/19/2005

TIME: 08:40:41

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\04192005\J506327.raw

3 <110> APPLICANT: HIRAMATSU, Shingo
 4 TANAKA, Takashi
 5 YAMADA, Katsushige
 6 TAMURA, Toshiki
 8 <120> TITLE OF INVENTION: PRODUCTION OF PHYSIOLOGICALLY ACTIVE PROTEINS USING GENE
 RECOMBINANT
 9 SILKWORMS
 11 <130> FILE REFERENCE: 0210-0190PUS1
 13 <140> CURRENT APPLICATION NUMBER: US 10/506,327
 14 <141> CURRENT FILING DATE: 2004-09-02
 16 <150> PRIOR APPLICATION NUMBER: PCT/JP03/02675
 17 <151> PRIOR FILING DATE: 2003-03-06
 19 <160> NUMBER OF SEQ ID NOS: 38
 21 <170> SOFTWARE: Patent-In 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1910
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: sericin-1 gene promoter-feline interferon-w-bovine growth
 hormone poly A
 30 addition sequence
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1071)...(1652)
 37 <220> FEATURE:
 38 <221> NAME/KEY: sig_peptide
 39 <222> LOCATION: (1071)...(1139)
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 42 <221> NAME/KEY: mat_peptide
 43 <222> LOCATION: (1140)...(1652)
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 47 tatccaaata ttattcgtgt attgtttata gcctttgtca agtcttttac aaggcaagat 120
 48 aataagtaat attccgtgat tggacgtaac atttcccgga agatccttag ccgataagtc 180
 49 gaagagccgc atgtggctag agagacgcgg gtttccgacc actggccttag gcgcttattc 240
 50 cgccataata gatgtacgtg ttcacaatta gcacccgaaa ttcgtaatag ctacgagaag 300
 51 tatcgaatat caaaaatcta tatattaata cgtgaagcaa aaactttgta tcccttttta 360
 52 cgaaaattgc gaggacggag gagtatgaaa tttcccacac ttatagagaa tacagagaag 420
 53 aagtgcacaa tgctaataatt tttttaaaat aatgcataaa agatacttta aatcaataaa 480
 54 gaaaacagca cacacactac ataccatgta tttgacgcac acacgcatgt atactattta 540
 55 ttgtcaaact tttgttcttg acgtctgtgt tcaaactgag aatagattaa atattgtttg 600
 56 tctttattaa tatttttttaa tagtgtagtc ttggcgaaat ttgtgattat agaagtataa 660
 57 aatacaatca taatagtgtg caaacttaca attcccaatt aattatagtc gaatttcgac 720

58 tactgcggga cctctagtat taataattct ctttaaaaaa aaacagagca tcaaatactg 780

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59 tcacaaatgt caagcgggtc tcaacgagcc atgaataaat tagaaatcaa ttaataacat 840
60 aaaataggca aacaaaataa aaccatttac atagagaacg tttgttgaac aaaaacaata 900
61 acttgtatac attgtttgca caaatgtttg aaccgaaaat ttattactct ctacgtaagc 960
62 ttgatcaaac ttcgttttcg tataaaacgc gttggcccaa ccactttggc atagtcgtct 1020
63 tatcatcggg tctctaagga tcaagcgatc caagaccgc caacgtcgac atg gcg 1076
64                                     Met Ala
65                                     1
66 ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc aac tcc 1124
67 Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys Asn Ser
68           5                10                15
69 gtc tgc gtg ctg ggc tgt gac ctg cct cag acc cac ggc ctg ctg aac 1172
70 Val Cys Val Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn
71       20                25                30
72 agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct gcc agc 1220
73 Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser
74 35                40                45                50
75 tcc tgt cag aag gac aga aat gac ttc gcc ttc ccc cag gac gtg ttc 1268
76 Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe
77           55                60                65
78 ggt gga gac cag tcc cac aag gcc caa gcc ctc tcg gtg gtg cac gtg 1316
79 Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val His Val
80           70                75                80
81 acg aac cag aag atc ttc cac ttc ttc tgc aca gag gcg tcc tcg tct 1364
82 Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser
83           85                90                95
84 gct gct tgg aac acc acc ctc ctg gag gaa ttt tgc acg gga ctt gat 1412
85 Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp
86       100                105                110
87 cgg cag ctg acc cgc ctg gaa gcc tgt gtc ctg cag gag gtg gag gag 1460
88 Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu
89 115                120                125                130
90 gga gag gct ccc ctg acg aac gag gac att cat ccc gag gac tcc atc 1508
91 Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile
92           135                140                145
93 ctg agg aac tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa 1556
94 Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys
95           150                155                160
96 tac agc cct tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc 1604
97 Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser
98       165                170                175
99 ttg tat tat tca tca aca gcc ttg cag aaa aga tta agg agc gag aaa 1652
100 Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
101       180                185                190
102 tga tctagaccgc tgatcagcct cgactgtgcc ttctagttgc cagccatctg 1705
103 ttgtttgccc ctccccgtg ccttccttga ccctggaagg tgccactccc actgtccttt 1765
104 cctaataaaa tgaggaaatt gcatcgcatc gtctgagtag gtgtcattct attctggggg 1825
105 gtgggggtggg gcaggacagc aagggggagg attgggaaga caatagcagg catgctgggg 1885
106 atgcggtggg ctctatggcc tcgag 1910
108 <210> SEQ ID NO: 2

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109 <211> LENGTH: 1172
 110 <212> TYPE: DNA
 111 <213> ORGANISM: Artificial Sequence
 113 <220> FEATURE:
 114 <223> OTHER INFORMATION: fibroin H chain gene promoter-feline interferon-w-bovine growth hormone
 115 poly A addition sequence
 117 <220> FEATURE:
 118 <221> NAME/KEY: CDS
 119 <222> LOCATION: (333)...(914)
 121 <220> FEATURE:
 122 <221> NAME/KEY: sig_peptide
 123 <222> LOCATION: (333)...(401)
 125 <220> FEATURE:
 126 <221> NAME/KEY: mat_peptide
 127 <222> LOCATION: (402)...(914)
 129 <400> SEQUENCE: 2
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 131 ataaaattct ttaaaatatt aaaagtaaga acaataagat caattaaatc ataattaatc 120
 132 acattgttca tgatcacaat ttaatttact tcatacgttg tattgttatg ttaaataaaa 180
 133 agattaattt ctatgtaatt gtatctgtac aatacaatgt gtagatgttt attctatcga 240
 134 aagtaaatac gtcaaaactc gaaaattttc agtataaaaa gggttcaactt tttcaaataca 300
 135 gcatcagttc gggtccaact ctcaagggtcg ac atg gcg ctg ccc tct tcc ttc 353
 136 Met Ala Leu Pro Ser Ser Phe
 137 1 5
 138 ttg gtg gcc ctg gtg gcg ctg ggc tgc aac tcc gtc tgc gtg ctg ggc 401
 139 Leu Val Ala Leu Val Ala Leu Gly Cys Asn Ser Val Cys Val Leu Gly
 140 10 15 20
 141 tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 449
 142 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
 143 25 30 35
 144 ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac 497
 145 Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
 146 40 45 50 55
 147 aga aat gac ttc gcc ttc ccc cag gac gtg ttc ggt gga gac cag tcc 545
 148 Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 149 60 65 70
 150 cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc 593
 151 His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
 152 75 80 85
 153 ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc 641
 154 Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
 155 90 95 100
 156 acc ctc ctg gag gaa ttt tgc acg gga ctt gat cgg cag ctg acc cgc 689
 157 Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg
 158 105 110 115
 159 ctg gaa gcc tgt gtc ctg cag gag gtg gag gag gga gag gct ccc ctg 737
 160 Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu Ala Pro Leu
 161 120 125 130 135
 162 acg aac gag gac att cat ccc gag gac tcc atc ctg agg aac tac ttc 785

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163 Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr Phe
164                               140                               145                               150
165 caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct tgt gcc      833
166 Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala
167                               155                               160                               165
168 tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat tca tca      881
169 Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser
170                               170                               175                               180
171 aca gcc ttg cag aaa aga tta agg agc gag aaa tga tctagaccgc      927
172 Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
173      185                               190
174 tgatcagcct cgactgtgcc ttctagttgc cagccatctg ttgtttgccc ctcccccggtg      987
175 ccttccttga ccctggaagg tgccactccc actgtccttt cctaataaaa tgaggaaatt      1047
176 gcatcgcatt gtctgagtag gtgtcattct attctggggg gtgggggtggg gcaggacagc      1107
177 aaggggggagg attgggaaga caatagcagg catgctgggg atgcggtggg ctctatggcc      1167
178 tcgag      1172
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181 <211> LENGTH: 31
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Synthesized oligonucleotide used in PCR to acquire the
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187      gene
189 <400> SEQUENCE: 3
190 acgcgtcgac atgggcgctg ccctcttct t      31
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 30
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Synthesized oligonucleotide used in PCR to acquire the
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199      gene
201 <400> SEQUENCE: 4
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204 <210> SEQ ID NO: 5
205 <211> LENGTH: 29
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Synthesized oligonucleotide used in PCR to acquire the
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211      promoter
213 <400> SEQUENCE: 5
214 ccggaattcg gtcagaaacc ttgttaacc      29
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 30
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Synthesized oligonucleotide used in PCR to acquire the
sericin-1 gene

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223      promoter
225 <400> SEQUENCE: 6
226 acgcgtcgac gttggcggtc tttggatcgc          30
228 <210> SEQ ID NO: 7
229 <211> LENGTH: 29
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Synthesized oligonucleotide used in PCR to acquire the
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235      gene promoter
237 <400> SEQUENCE: 7
238 ccggaattcg ggagaaagca tgaagtaag          29
240 <210> SEQ ID NO: 8
241 <211> LENGTH: 30
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Synthesized oligonucleotide used in PCR to acquire the
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247      gene promoter
249 <400> SEQUENCE: 8
250 acgcgtcgac cttgagagtt ggaaccgaac          30
252 <210> SEQ ID NO: 9
253 <211> LENGTH: 30
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Synthesized oligonucleotide used in PCR to acquire the
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259      hormone gene poly A
261 <400> SEQUENCE: 9
262 ctagtctaga ccgctgatca gcctcgactg          30
264 <210> SEQ ID NO: 10
265 <211> LENGTH: 30
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Synthesized oligonucleotide used in PCR to acquire the
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271      hormone gene poly A
273 <400> SEQUENCE: 10
274 cgcggatccg ccatagagcc caccgcatcc          30
276 <210> SEQ ID NO: 11
277 <211> LENGTH: 34
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Synthesized oligonucleotide used in PCR as a primer with a
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283      solution of sericin-1 gene fragment, feline interferon-w gene fragment, and
284      bovine growth hormone poly A
286 <400> SEQUENCE: 11

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287 gacctcgagg gtcagaaacc ttgttaacca atag

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 04/19/2005

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Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\04192005\J506327.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:3; Line(s) 186
Seq#:4; Line(s) 198
Seq#:17; Line(s) 415
Seq#:31; Line(s) 890
Seq#:35; Line(s) 938
Seq#:36; Line(s) 951

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/506,327

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Input Set : A:\PTO.SR.txt

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